

wherein said first substrate binding region has a sequence complementary to a first portion of said preselected substrate nucleic acid sequence,

said second substrate binding region has a sequence complementary to a second portion of said preselected substrate nucleic acid sequence, and

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said core region having a sequence according to the formula:

(I.) T(stem)'AGC(stem)"Z,

wherein said (stem)' and (stem)" are each three sequential nucleotides which when hybridized as a (stem)':(stem)" pair comprise three base pairs including at least two G:C pairs and wherein said Z = WCGR or WCGAA, and W = A or T and R = A or G; or

(II.) RGGCTAGCHACAACGA (SEQ ID NO 122),

wherein said H = T, C or A, and R = A or G.

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29. A method of engineering a catalytic DNA molecule that cleaves a preselected substrate nucleic acid sequence in a target nucleic acid molecule, comprising the steps of:

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a) selecting a substrate nucleic acid sequence of from 10 to 26 nucleotides in length in a target nucleic acid molecule; and

b) synthesizing a deoxyribonucleic acid molecule comprising first and second substrate binding regions flanking a core region,

wherein said first substrate binding region has a sequence complementary to a first portion of said preselected nucleic acid target sequence,

said second substrate binding region has a sequence